SEQUENCE LISTING

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<110>	Scadden, David T. Poznansky, Mark C. Olszak, Ivona T. Brown, Edward M.														
<120>	THE CaR RECEPTOR AS A MEDIATOR OF MIGRATORY CELL CHEMOTAXIS AND/OR CHEMOKINESIS														
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	tct Ser															436
	acg Thr		_				_					~		_	_	484
	gca Ala		_	-							_	-			-	532
	tcc Ser 170															580
_	acc Thr				_			_	_		_	_	_	_		628
	gag Glu															676
_	tat Tyr			_						_		_	_		_	724
	gat Asp		-		_		_	-				_			_	772
	gag Glu 250			_			-							_	_	820
	gtc Val			_			-			-						868
_	gag Glu		_		_			_		_			_	_	_	916
	gcc Ala		_	_			_		-	_		-				964
	gtt Val							_	_	_	-		_			1012
	ttc Phe 330		_		_	_	_	_				-		_		1060
	ggt Gly															1108
caa	gaa	ggt	gca	aaa	gga	cct	tta	cct	gtg	gac	acc	ttt	ctg	aga	ggt	1156

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I	ccc Pro	ctc Leu	tgt Cys 395	aca Thr	ggg Gly	gat Asp	gag Glu	aac Asn 400	atc Ile	agc Ser	agt Ser	gtc Val	gag Glu 405	acc Thr	cct Pro	tac Tyr	1252
ā	ata [le	gat Asp 410	tac Tyr	acg Thr	cat His	tta Leu	cgg Arg 415	ata Ile	tcc Ser	tac Tyr	aat Asn	gtg Val 420	tac Tyr	tta Leu	gca Ala	gtc Val	1300
1	ac Yr 125	tcc Ser	att Ile	gcc Ala	cac His	gcc Ala 430	ttg Leu	caa Gln	gat Asp	ata Ile	tat Tyr 435	acc Thr	tgc Cys	tta Leu	cct Pro	ggg Gly 440	1348
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t	at 'yr	tcc Ser 490	atc Ile	atc Ile	aac Asn	tgg Trp	cac His 495	ctc Leu	tcc Ser	cca Pro	gag Glu	gat Asp 500	ggc Gly	tcc Ser	atc Ile	gtg Val	1540
F	tt he 05	aag Lys	gaa Glu	gtc Val	ggg Gly	tat Tyr 510	tac Tyr	aac Asn	gtc Val	tat Tyr	gcc Ala 515	aag Lys	aag Lys	gga Gly	gaa Glu	aga Arg 520	1588
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a L	ag ys	gag Glu	atc Ile	gag Glu	ttt Phe 605	ctg Leu	tcg Ser	tgg Trp	acg Thr	gag Glu 610	ccc Pro	ttt Phe	Gly ggg	atc Ile	gca Ala 615	ctc Leu	1876

acc Thr	ctc Leu	ttt Phe	gcc Ala 620	gtg Val	ctg Leu	ggc Gly	att Ile	ttc Phe 625	ctg Leu	aca Thr	gcc Ala	ttt Phe	gtg Val 630	ctg Leu	ggt Gly	192	4
gtg Val	ttt Phe	atc Ile 635	aag Lys	ttc Phe	cgc Arg	aac Asn	aca Thr 640	ccc Pro	att Ile	gtc Val	aag Lys	gcc Ala 645	acc Thr	aac Asn	cga Arg	197	2
gag Glu	ctc Leu 650	tcc Ser	tac Tyr	ctc Leu	ctc Leu	ctc Leu 655	ttc Phe	tcc Ser	ctg Leu	ctc Leu	tgc Cys 660	tgc Cys	ttc Phe	tcc Ser	agc Ser	202	0
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cag Gln	ccg Pro	gcc Ala	ttt Phe	ggc Gly 685	atc Ile	agc Ser	ttc Phe	gtg Val	ctc Leu 690	tgc Cys	atc Ile	tca Ser	tgc Cys	atc Ile 695	ctg Leu	211	.6
gtg Val	aaa Lys	acc Thr	aac Asn 700	cgt Arg	gtc Val	ctc Leu	ctg Leu	gtg Val 705	ttt Phe	gag Glu	gcc Ala	aag Lys	atc Ile 710	ccc Pro	acc Thr	216	54
agc Ser	ttc Phe	cac His 715	cgc Arg	aag Lys	tgg Trp	tgg Trp	ggg Gly 720	ctc Leu	aac Asn	ctg Leu	cag Gln	ttc Phe 725	ctg Leu	ctg Leu	gtt Val	221	.2
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aag Lys	tcc Ser	cgg Arg 795	l Lys	ctg Leu	ccg Pro	gag Glu	aac Asn 800	Phe	aat Asn	gaa Glu	gcc Ala	aag Lys 805	Phe	atc	acc	245	52
ttc Phe	ago Ser 810	Met	cto Leu	ato Ile	ttc Phe	Phe 815	Ile	gtc Val	tgg Trp	g ato	tcc Ser 820	Phe	att Ile	cca Pro	gcc Ala	25	00
tat Tyr 825	Ala	ago Sei	c acc	tat Tyr	ggc Gly 830	Lys	ttt Phe	gto Val	c tct L Ser	gcc Ala 835	ı Val	a gag L Glu	gtç Val	att Ile	gcc Ala 840	25	48
ato Ile	cto Lev	g gca ı Ala	a gco a Ala	ago Ser 845	: Phe	: ggc	tto Lei	g cto 1 Lei	g gcg ı Ala 850	а Суз	c ato	tto Phe	tto Phe	aac Asr 855	aag Lys	25	96
acc	tac	c ato	c att	cto	c tto	aaq	g cca	a tco	c cgo	c aad	c aco	c ato	gag	g gag	g gtg	26	44

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cgt Arg	tgc Cys	agc Ser 875	acc Thr	gca Ala	cgt Arg	cac His	gct Ala 880	ttc Phe	aag Lys	gtg Val	gct Ala	gcc Ala 885	cgg Arg	gcc Ala	acg Thr	2692
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tcc Ser 905	acg Thr	gga Gly	tcc Ser	acc Thr	ccc Pro 910	tcc Ser	tcc Ser	tcc Ser	atc Ile	agc Ser 915	agc Ser	aag Lys	agc Ser	aac Asn	agc Ser 920	2788
gaa Glu	gac Asp	cca Pro	ttc Phe	cca Pro 925	cag Gln	ccc Pro	gag Glu	agg Arg	cag Gln 930	aag Lys	cag Gln	cag Gln	cag Gln	ccg Pro 935	ctg Leu	2836
gcc Ala	cta Leu	acc Thr	cag Gln 940	caa Gln	gag Glu	cag Gln	cag Gln	cag Gln 945	cag Gln	ccc Pro	ctg Leu	acc Thr	ctc Leu 950	cca Pro	cag Gln	2884
cag Gln	caa Gln	cga Arg 955	tct Ser	cag Gln	cag Gln	cag Gln	ccc Pro 960	aga Arg	tgc Cys	aag Lys	cag Gln	aag Lys 965	gtc Val	atc Ile	ttt Phe	2932
ggc	agc Ser 970	ggc Gly	acg Thr	gtc Val	acc Thr	ttc Phe 975	tca Ser	ctg Leu	agc Ser	ttt Phe	gat Asp 980	gag Glu	cct Pro	cag Gln	aag Lys	2980
aac Asn 985	gcc Ala	atg Met	gcc Ala	cac His	agg Arg 990	aat Asn	tct Ser	acg Thr	cac His	cag Gln 995	aac Asn	tcc Ser	ctg Leu	Glu	gcc Ala .000	3028
cag Gln	aaa Lys	agc Ser	Ser	gat Asp .005	acg Thr	ctg Leu	acc Thr	Arg	cac His .010	cag Gln	cca Pro	tta Leu	Leu	ccg Pro .015	ctg Leu	3076
cag Gln	tgc Cys	Gly	Glu	Thr	gac Asp	Leu	Asp	Leu	Thr	gtc Val	cag Gln	gaa Glu 1	aca Thr 030	ggt Gly	ctg Leu	3124
caa Gln	Gly	cct Pro .035	gtg Val	ggt Gly	gga Gly	Asp	cag Gln 040	cgg Arg	cca Pro	gag Glu	Val	gag Glu .045	gac Asp	cct Pro	gaa Glu	3172
Glu	ttg Leu 050	tcc Ser	cca Pro	gca Ala	Leu	gta Val 055	gtg Val	tcc Ser	agt Ser	Ser	cag Gln 060	agc Ser	ttt Phe	gtc Val	atc Ile	3220
agt Ser 065	ggt Gly	gga Gly	ggc Gly	Ser	act Thr 070	gtt Val	aca Thr	gaa Glu	Asn	gta Val 075	gtg Val	aat Asn	tca Ser			3262
taaa gatg	atgg agga	aa g at c	gaga gccc	agac caga	t gg c tc	gcta cttt	ggga cctc	gaa tga	tgca ggaa	gag ga	aggt	ttct	tg g	ggtc	ccagg	3322 3361
	<2 <2	10> 11> 12> 13>	1078 PRT		iens											

<220>
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<223> Ca-sensing Receptor

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Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe 645 650 Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro 665 670 Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile Val Ile Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn Gln Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala Cys Ile Phe Phe Asn Lys Thr Tyr Ile Ile Leu Phe Lys Pro Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Arg His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Gln Gln Gln

930 935 Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro 950 955 960 Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser 965 970 975 Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Arg Asn Ser 980 985 990 Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr 995 1000 1005 Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp 1010 1015 1020 Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln 1030 1035 104 Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val 1045 1050 1055 Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Ser Thr Val Thr 1060 1065 1070 Glu Asn Val Val Asn Ser 1075